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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Tue May 22 09:08:03 EDT 2007

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Application No: 10574085 Version No: 1.0

Input Set:

Output Set:

Started: 2007-05-21 11:28:46.134
Finished: 2007-05-21 11:28:46.514
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 380 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)

SEQUENCE LISTING

<110> Sode, Koji

<120> GLUCOSE DEHYDROGENASE/CYTOCHROME FUSION PROTEIN

<130> 3691-0130PUS1

<140> 10574085

<141> 2007-05-21

<150> US 10/574,085

<151> 2006-03-30

<150> PCT/JP2004/014575

<151> 2004-09-28

<150> JP 2003-340092

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA coding for a fusion protein

<400> 1

atgaataaaac	atttattggc	taaaaattgct	ttattaagcg	ctgttcagct	agttacactc	60
tcagcatttgc	ctgatgttcc	tctaactcca	tctcaatttg	ctaaagcgaa	atcagagaac	120
tttgacaaga	aagtatttct	atctaatactca	aataagccgc	atgctttgtt	atggggacca	180
gataatcaaa	tttggtaaac	tgagcgagca	acaggttaaga	ttcttaagagt	taatccagag	240
tcgggttagtg	taaaaaacagt	tttcaggtta	ccagagattg	tcaatgatgc	tgtatggcag	300
aatggtttat	taggtttgc	cttccatct	gatttaaaa	ataatcctta	tatctatatt	360
tcaggtacat	ttaaaaatcc	gaaatctaca	gataaagaat	taccgaacca	aacgattatt	420
cgtcgttata	cctataataa	atcaacagat	acgctcgaga	agccagtctga	tttatttagca	480
ggattacctt	catcaaaaga	ccatcagtca	ggtcgtcttg	tcatttggcc	agatcaaaag	540
atttattata	cgatttggta	ccaaaggcgt	aaccagctt	cttatttgtt	cttgccaaat	600
caaggcacaac	atacccaaac	tcaacaagaa	ctgaatggta	aagactatca	cacctatatg	660
ggtaaagtac	tacgctaaa	tcttgatgga	agtattccaa	aggataatcc	aagtttaac	720
gggggtggta	ccatattta	tacacttgg	catcgtatc	cgcagggtt	agcattcact	780
ccaaatggta	aattattgca	gtctgaacaa	ggcccaaact	ctgacgatga	aattaacctc	840
attgtcaaag	gtggcaatta	tgggtggcc	aatgttagcag	gttataaaaga	tgatagtgcc	900
tatgcttatg	caaattattc	agcagcagcc	aataagtcaa	ttaaggattt	agctcaaaat	960
ggagtaaaag	tagccgcagg	ggtccctgtt	acgaaagaat	ctgaatggac	tggtaaaaac	1020
tttgtccac	cattaaaaac	tttatatacc	gttcaagata	cctacaacta	taacgatcca	1080
acttgtggag	agatgaccta	catttgcgtt	ccaacagttt	caccgtcatc	tgcctatgtc	1140
tataaggcgc	gtaaaaaaagc	aattacttgt	tggggaaaata	cattatggt	tccatcttta	1200
aaacgtgggt	tcattttccg	tattaagttt	gatccaactt	atagcactac	ttatgtatgac	1260
gctgtaccga	tgtttaagag	caacaaccgt	tatcgtatgt	tgatttgcag	tccagatgg	1320
aatgtcttat	atgttataac	tgtatctgtcc	ggaaatgtcc	aaaaagatga	tggctcgtta	1380
acaatacat	tagaaaaaccc	aggatctctc	attaagttca	cctataaggc	taaggagctc	1440

ggcaaggcca ggatgccgga gttcggtggcc cagcgacccg gccagttgt gcagggcgtg	1500
aaatacggacc ccgccaagggt cgaggccggc accatgtgt atgtggccaa ctgcgttttc	1560
tgtcacggcg tgcctggcg ggaccgtggc ggaaacattc ccaatctggg ttacatggac	1620
gcgagctata tcgagaacctt gcttcaagg gccggccat ggtgcgcggc	1680
atgcggact tcacggcaa gttgtcgggc gatgacgtgg agtccctcaa ggccttcatc	1740
cagggcacgg cggacgccc catccgcccag ccctga	1776

<210> 2
 <211> 591
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic fusion protein

Met Asn Lys His Leu Leu Ala Lys Ile Ala Leu Leu Ser Ala Val Gln			
1	5	10	15
Leu Val Thr Leu Ser Ala Phe Ala Asp Val Pro Leu Thr Pro Ser Gln			
20	25	30	
Phe Ala Lys Ala Lys Ser Glu Asn Phe Asp Lys Lys Val Ile Leu Ser			
35	40	45	
Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln Ile			
50	55	60	
Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro Glu			
65	70	75	80
Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn Asp			
85	90	95	
Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp Phe			
100	105	110	
Lys Asn Asn Pro Tyr Ile Tyr Ile Ser Gly Thr Phe Lys Asn Pro Lys			
115	120	125	
Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr Thr			
130	135	140	
Tyr Asn Lys Ser Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu Ala			
145	150	155	160
Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile Gly			
165	170	175	
Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Arg Asn Gln			
180	185	190	
Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala Gln His Thr Pro Thr Gln			
195	200	205	
Gln Glu Leu Asn Gly Lys Asp Tyr His Thr Tyr Met Gly Lys Val Leu			
210	215	220	
Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys Asp Asn Pro Ser Phe Asn			
225	230	235	240
Gly Val Val Ser His Ile Tyr Thr Leu Gly His Arg Asn Pro Gln Gly			
245	250	255	
Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu Gln Ser Glu Gln Gly Pro			
260	265	270	
Asn Ser Asp Asp Glu Ile Asn Leu Ile Val Lys Gly Gly Asn Tyr Gly			
275	280	285	
Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp Ser Gly Tyr Ala Tyr Ala			
290	295	300	
Asn Tyr Ser Ala Ala Ala Asn Lys Ser Ile Lys Asp Leu Ala Gln Asn			
305	310	315	320

Gly Val Lys Val Ala Ala Gly Val Pro Val Thr Lys Glu Ser Glu Trp
 325 330 335
 Thr Gly Lys Asn Phe Val Pro Pro Leu Lys Thr Leu Tyr Thr Val Gln
 340 345 350
 Asp Thr Tyr Asn Tyr Asn Asp Pro Thr Cys Gly Glu Met Thr Tyr Ile
 355 360 365
 Cys Trp Pro Thr Val Ala Pro Ser Ser Ala Tyr Val Tyr Lys Gly Gly
 370 375 380
 Lys Lys Ala Ile Thr Gly Trp Glu Asn Thr Leu Leu Val Pro Ser Leu
 385 390 395 400
 Lys Arg Gly Val Ile Phe Arg Ile Lys Leu Asp Pro Thr Tyr Ser Thr
 405 410 415
 Thr Tyr Asp Asp Ala Val Pro Met Phe Lys Ser Asn Asn Arg Tyr Arg
 420 425 430
 Asp Val Ile Ala Ser Pro Asp Gly Asn Val Leu Tyr Val Leu Thr Asp
 435 440 445
 Thr Ala Gly Asn Val Gln Lys Asp Asp Gly Ser Val Thr Asn Thr Leu
 450 455 460
 Glu Asn Pro Gly Ser Leu Ile Lys Phe Thr Tyr Lys Ala Lys Glu Leu
 465 470 475 480
 Gly Lys Ala Arg Met Pro Glu Phe Val Ala Gln Arg Thr Gly Gln Leu
 485 490 495
 Leu Gln Gly Val Lys Tyr Asp Pro Ala Lys Val Glu Ala Gly Thr Met
 500 505 510
 Leu Tyr Val Ala Asn Cys Val Phe Cys His Gly Val Pro Gly Val Asp
 515 520 525
 Arg Gly Gly Asn Ile Pro Asn Leu Gly Tyr Met Asp Ala Ser Tyr Ile
 530 535 540
 Glu Asn Leu Pro Asn Phe Val Phe Lys Gly Pro Ala Met Val Arg Gly
 545 550 555 560
 Met Pro Asp Phe Thr Gly Lys Leu Ser Gly Asp Asp Val Glu Ser Leu
 565 570 575
 Lys Ala Phe Ile Gln Gly Thr Ala Asp Ala Ile Arg Pro Lys Pro
 580 585 590

<210> 3
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 3
 ggccatggat aaacatttat tggctaaaat tgctttat

38

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 4
 gggggagctc cttagcctta taggtgaac

29

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 5
gggggagctc ggcaaggcca ggatgccgga 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 6
ggggaagctt tcaggccttg ggccggatgg 30